
WIPREH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu May 6 15:08:47 1999; MagPar time 1644.23 Seconds
Tabular output not generated. 1384.282 Million cell updates/sec

Title: >US-09-037-460-1
Description: (1-1271) from US09037460.seq
Perfect Score: 1266
N.A. Sequence: 1 CTGCTTCCACGACGAAAGA.....GTTCCTTNTCTNAAGGAC 1271
Comp: GACGAAGGTGGTCGCTTCTT.....CAANGGANAGANTTCCTG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-est56
Database: genbank-est109
1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est20 17:gb_est21
18:gb_est22 19:gb_est23 20:gb_est24 21:gb_est25 22:gb_est26
23:gb_est27 24:gb_est28 25:gb_est29 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 11.873; Variance 3.231; scale 3.674

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	412	32.5	425	21	W46667	0.00e+00
2	139	11.0	351	24	AA296697	1.44e-152
3	62	4.9	252	12	ESN112419	1.37e-44
4	56	4.4	252	12	AA754459	5.86e-37
5	48	3.8	247	12	AA754458	5.86e-37
6	46	3.6	247	12	AA754458	5.86e-37
7	35	2.8	2275	11	AF034173	5.24e-24
8	33	2.6	236	11	AF034173	5.24e-24
9	30	2.4	467	29	AA0151727	5.83e-10
10	29	2.3	199	14	AA926494	7.59e-07
11	29	2.3	265	15	AA005619	7.20e-06
12	29	2.3	284	14	AA890895	7.20e-06
13	29	2.3	369	10	AA642307	7.20e-06

14	29	2.3	369	11	AA670056	ag39h07.sl	Jia bone ma	7.20e-06
15	29	2.3	379	10	AA620322	af09g06.sl	Soares test	7.20e-06
16	29	2.3	399	17	AI038446	ow21d11.xl	Soares para	7.20e-06
17	29	2.3	420	8	AA397891	zt86c04.rl	Soares test	7.20e-06
18	29	2.3	421	8	AA494213	ng99g03.sl	NCI_CGAP.Th	7.20e-06
19	29	2.3	433	15	AI003780	ou91g01.xl	NCI_CGAP_Ki	7.20e-06
20	29	2.3	441	19	N72081	yz97d02.sl	Homo sapien	7.20e-06
21	29	2.3	451	8	AA126449	zn85e12.sl	Stratagene	7.20e-06
22	29	2.3	469	6	CO5912	similar to none	mRNA	7.20e-06
23	29	2.3	499	15	AI041163	ov59g09.xl	Soares test	7.20e-06
24	29	2.3	555	20	AA001197	ze48e12.sl	Soares reti	7.20e-06
25	29	2.3	719	14	AA950736	LD30843.5prime	LD Dros	7.20e-06
26	28	2.2	275	12	AA789162	ag58a11.sl	Gessler Will	6.51e-05
27	28	2.2	280	13	AA830387	oc48h08.sl	NCI_CGAP_GC	6.51e-05
28	28	2.2	332	11	AA580607	nc80b11.sl	NCI_CGAP_GC	6.51e-05
29	28	2.2	343	11	AA719452	zh35h07.sl	Soares pine	6.51e-05
30	28	2.2	356	7	HUM215G05B	Human aorta	cDNA 5'-en	6.51e-05
31	28	2.2	361	8	AA233919	zr49e02.sl	Soares NHM	6.51e-05
32	28	2.2	364	13	AA804446	nz38c06.sl	NCI_CGAP_GC	6.51e-05
33	28	2.2	375	15	AI049727	an37c10.xl	Gessler Will	6.51e-05
34	28	2.2	409	10	AA653384	ag55h03.sl	Gessler Will	6.51e-05
35	28	2.2	416	21	W65422	z33b05.sl	Soares feta	6.51e-05
36	28	2.2	426	10	AA625676	zu86a05.sl	Soares test	6.51e-05
37	28	2.2	430	11	AA662165	ns66c08.sl	NCI_CGAP_Pr	6.51e-05
38	28	2.2	430	10	AA614832	nn96c07.sl	NCI_CGAP_Pr	6.51e-05
39	28	2.2	437	8	AA234168	zr49e02.sl	Soares NHM	6.51e-05
40	28	2.2	441	14	H92123	ys84h01.rl	Homo sapien	6.51e-05
41	28	2.2	441	14	AA902495	ok91h09.sl	NCI_CGAP_Lu	6.51e-05
42	28	2.2	496	13	AA868954	ak55e05.sl	Soares test	6.51e-05
43	28	2.2	522	22	AA204900	zg61a09.rl	Stratagene	6.51e-05
44	28	2.2	614	14	AA898668	NCM7G1T7	Mycelial Neur	6.51e-05
45	28	2.2	748	15	C93732	Dictyostellum	discoide	6.51e-05

ALIGNMENTS

RESULT	1	W46667	425 bp	mRNA	EST	11-OCT-1996
LOCUS	zc33e02.r1	Soares senescent fibroblasts	NbHSF	Homo sapiens	CDNA	
DEFINITION	clone 324122	5', mRNA sequence.				
ACCESSION	W46667					
NID	91331295					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
AUTHORS	1 (bases 1 to 425) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasaki, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.					
TITLE	The WashU-Merck EST Project					
JOURNAL	Unpublished (1995)					
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1322 Std Error: 0.00 Seq primer: mob.REGA-ET High quality sequence stop: 395. Location/Qualifiers 1. .425 /organism="Homo sapiens" /note="Vector: pT73D (Pharmacia) with a modified polylinker V_Type: phagemid; Site_1: Not I; Site_2: Eco					

FEATURES

Source

RI: TGTTACCAATCTGAAGTGGAGCGCGCCATTTTTTTTTTTTTTTTTTTT
 3'], double-stranded cDNA was size selected, ligated to
 Eco RI adapters (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pT73
 vector (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo.
 /db_xref="taxon:9606"
 /clone="324122"
 /clone_lib="Soares senescent fibroblasts NBHSF"
 /tissue_type="senescent fibroblast"
 /lab_host="DH10B (ampicillin resistant)"
 <1..>425
 144 a 50 c 102 g 126 t 3 others
 MEDLINE
 COMMENT

Query Match 32.5%; Score 412; DB 21; Length 425;
 Best Local Similarity 98.1%; Pred. No. 0.00e+00;
 Matches 417; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 Db 1 GTTAAATTCGAATGATGATGATTTTAAATGTTGTGTATAGTAACTGAAGAAC 60
 Qy 812 GTTAAATTCGAATGATGATGATTTTAAATGTTGTGTATAGTAACTGAAGAAC 871
 Db 61 TAAAAATGCAATTTAGTAACTTTACATGGAGACAGTCAACCAAGAGGAGCTAGGCA 120
 Qy 872 TAAAAATGCAATTTAGTAACTTTACATGGAGACAGTCAACCAAGAGGAGCTAGGCA 931
 Db 121 AAGCTGAAGACCGCAGTCAGTCAATAGTTCTTTTGTAGTTGATGATTAATGTTGGG 180
 Qy 932 AAGCTGAAGACCGCAGTCAGTCAATAGTTCTTTTGTAGTTGATGATTAATGTTGGG 991
 Db 181 ATATGGAATGAAGACTTAAGACGAGGAGATGCGNNAGGGGTGGGAGTGGGAATAAA 240
 Qy 992 ATATGGAATGAAGACTTAAGACGAGGAGATGCGGGGGGTGGGAGTGGGAATAAA 1051
 Db 241 ATATTTAGCCCTCTCTGTTAGTGTAGCTTCTAGATTTTAATATGCTTTTTTTTTT 300
 Qy 1052 ATATTTAGCCCTCTCTGTTAGTGTAGCTTCTAGATTTTAATATGCTTTTTTTTTT 1111
 Db 301 TTTTGGCTTTGGGAAAGTCAAAATTAACCAACCAAGAAACCCCTGAAGGAAGTAAGA 360
 Qy 1112 TTTTGGCTTTGGGAAAGTCAAAATTAACCAACCAAGAAACCCCTGAAGGAAGTAAGA 1170
 Db 361 TGTGAGCTTTATGAAATTTAGTAACTAACCAACAGCTTTGAAGTGAAGCAATTTCAAAA 420
 Qy 1171 TGTGAGCTTTATGAAATTTAGTAACTAACCAACAGCTTTGAAGTGAAGCAATTTCAAAA 1230
 Db 421 GGCTG 425
 Qy 1231 GGCTG 1235

RESULT 2 AA296697 351 bp mRNA EST 18-APR-1997
 LOCUS EST112419 Aorta endothelial cells, TNF alpha-treated Homo sapiens
 DEFINITION CDNA 5' end similar to endothelial cell-specific secretory
 molecule, mRNA sequence.
 ACCESSION AA296697
 NID 91949189
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
 Homo.
 1 (bases 1 to 351)
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,

Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 96026280
 Other_ESTs: TH0154673
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699055
 Fax: 3018699423
 Email: arkerlavet@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES

source Location/Qualifiers
 1..351
 /organism="Homo sapiens"
 /note="Organ: aorta; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"
 /db_xref="AACC (inhost):115698"
 /clone_lib="Aorta endothelial cells, TNF alpha-treated"
 /cell_type="endothelial cell"
 /dev_stage="adult"
 <1..>351
 BASE COUNT 118 a 57 c 72 g 102 t 2 others
 ORIGIN
 Query Match 11.0%; Score 139; DB 24; Length 351;
 Best Local Similarity 94.0%; Pred. No. 1.44e-152;
 Matches 140; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 Db 1 GGGAAAGTCAAATTAACACACCAAGAAACCCCTGAAGGAAGTAAGAGTTTGAAGCTT 60
 Qy 1123 GGGAAAGTCAAATTAACACACCAAGAAACCCCTGAAGGAAGTAAGAGTTTGAAGCTT 1182
 Db 61 ATGGAAATTTGAGTAACAAACAGCTTTGAACTGAGAGCAATTTCAAAGCGTCTGATCT 120
 Qy 1183 ATGGAAATTTGAGTAACAAACAGCTTTGAACTGAGAGCAATTTCAAAGCGTCTGATCT 1242
 Db 121 AGTTCGCGGTTACCTGATCTATCTGAAGGAC 149
 Qy 1243 AGCCCGCGGTTNCCTNTNTCTNAGGAC 1271

RESULT 3

LOCUS AA754459 252 bp mRNA EST 20-JAN-1998
 DEFINITION 97SN1787 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa
 ACCESSION AA754459
 NID 92801165
 KEYWORDS EST.
 SOURCE rice.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
 Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
 Poales; Poaceae; Oryza.
 1 (bases 1 to 252)
 REFERENCE Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
 Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,

Comp
In
San
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cp
Tel
Fax
Ema

BASE COUNT	77	a	63	c	63	g	62	t		
ORIGIN	/clone="IMAGE:1637415" /clone_lib="NCI_CGAP_GC3" /tissue_type="pooled germ cell tumors" /lab_host="DH10B" 77 a 63 c 63 g 62 t									
Query Match	2.3%	Score	29;	DB	15;	Length	265;			
Best Local Similarity	80.9%	Pred.	No. 7.20e-06;							
Matches	38;	Conservative	0;	Mismatches	9;	Indels	0;	Gaps 0;		
Db	7	GGTTTTTTTGGTTTTTGGTTTTTACC	CGCCGCCCAAAAAA	AAAAA	53					
Cp	1146	GGTGTATTATTTGACTTTTCCCAAGCCCAAAAAA	AAAAA	1100						
RESULT 12										
LOCUS	AA890895	284	bp	mRNA	EST	03-APR-1998				
DEFINITION	TENS0745	t. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 745 5', mRNA sequence.								
ACCESSION	AA890895									
NID	93017774									
KEYWORDS	EST.									
SOURCE	Trypanosoma cruzi.									
ORGANISM	Trypanosoma cruzi									
REFERENCE	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;									
AUTHORS	Trypanosoma; Schizotrypanum.									
TITLE	1 (bases 1 to 284)									
JOURNAL	Verdun, R.E., Di Paolo, N.C., Rondinelli, E., Frasch, A.C.C. and Sanchez, D.O.									
COMMENT	Gene discovery through EST sequencing in Trypanosoma cruzi Unpublished (1998)									
FEATURES	Contact: Sanchez D.O.									
source	Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral San Martin)									
	Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24 CP(1650) San Martin, Prov. de BS AS, Argentina									
	Tel: (54-1)752-9639 or (54-1)752-0021									
	Fax: (54-1)752-0021 or (54-1)752-9639									
	Email: dsanchez@inti.gov.ar									
	Seq primer: T7.									
	Location/Qualifiers									
	1..284									
	/organism="Trypanosoma cruzi"									
	/strain="Cl-Brenner"									
	/notes="cDNA library constructed with oligo dt primed epimastigote mRNA and cloned in pt7t318D phagemid with modified polylinker (PHARMACIA)"									
	/db_xref="taxon:5693"									
	/clone="745"									
	/clone_lib="t. cruzi epimastigote normalized cDNA Library"									
BASE COUNT	94	a	81	c	40	g	64	t		
ORIGIN	/cell_type="epimastigote" 5 others									
Query Match	2.3%	Score	29;	DB	14;	Length	284;			
Best Local Similarity	79.2%	Pred.	No. 7.20e-06;							
Matches	38;	Conservative	0;	Mismatches	10;	Indels	0;	Gaps 0;		
Db	13	GCATTTTTTTTTTTTTTTTTTTTGGTGGCAATAATAATAATAAAAAAC	60							
QY	1098	GCATTTTTTTTTTTTTTTTGGGCTTTGGGAAAGTCAAAATAAAACAC	1145							
RESULT 13										
LOCUS	AA642307	369	bp	mRNA	EST	27-OCT-1997				
DEFINITION	ns25b12.s1 NCI_CGAP_SCB1 Homo sapiens cDNA clone IMAGE:1184639 similar to contains element PTRS repetitive element ;, mRNA sequence.									
ACCESSION	AA642307									
NID	92567525									
KEYWORDS	EST.									

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo." /db xref="taxon:9606"

```

/clone="1030906"
/clone_lib="Soares testis NHT"
/sex="male"
/lab_host="DH10B"
71 C 50 g 115 t

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BASE COUNT	ORIGIN
143 a	71 c 50 g 115 t

Query Match 2.3%; Score 29; DB 10; Length 379;
Best Local Similarity 78.7%;
Pred. No. 7.20e-06;
Matches 37; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Db 257 TTTTGCCCTTGCAAGATCCAAAAAAGCACAAGTAA 303
 ||||| ||| | | ||||| ||||| ||||| : |||
 Cp 1136 TTTTGTACTTTTCCCAAGCCCAAAAAAAGCAYATTAA 1090

Search completed: Thu May 6 16:02:01 1999
Job time : 3194 secs.